

REMARKS

Claims 49-52, 56-60 and 64 are pending and under examination. Claims 49 and 57 have been amended. Support for the amendments can be found throughout the specification and claims as filed. Support for the amendment to claims 49 and 57, directed to determining open reading frames for genes or nucleotide sequences encoding gene products of unknown function in the microbe and assigning a function by determining homology to gene sequences encoding products of known function in a different organism can be found at, for example, page 7, second full paragraph, and in Figure 1. Accordingly, these amendments do not raise an issue of new matter and entry thereof is respectfully requested.

Interview Summary

Applicant and Applicant's representatives wish to thank Examiners Negin and Moran for the telephonic interview conducted on July 30, 2008. Applicant and Applicant's representatives discussed that one skilled in the art would not have combined the references cited under 35 U.S.C. § 103(a) to arrive at the claimed invention for the reasons of record. Applicant and Applicant's representatives discussed that any genes recited in Pramanik et al. were genes with known biochemical function in the organism being modeled. There is no teaching, suggestion or motivation in the cited combination of references to determine genes of unknown function and assign a function by homology to genes encoding products of known function in different organism to produce an *in silico* strain of a microbe as claimed.

An amendment to the independent claims directed to determining open reading frames of genes of unknown function in the microbe was suggested and viewed favorably by the Examiners. The claims have been amended above to include this element. Applicant and Applicant's representatives respectfully request consideration of this amendment with a view towards allowance. Should any minor considerations arise that may have been overlooked during the interview, Applicant and Applicant's representatives would appreciate the courtesy of addressing any such minor consideration by telephone interview or a supplemental submission in order to place this application in condition for allowance.

Rejections Under 35 U.S.C. § 103

Claims 49-52 and 56-60 stand rejected under 35 U.S.C. § 103(a) as allegedly obvious over Pramanik et al., Biotechnol. Bioengineer. 56:398-421 (1997), in view of Blattner et al., Science 277:1453-1469 (1997).

Applicant respectfully traverses for the reasons of record and those additionally discussed during the telephonic interview of July 30, 2008. Briefly, neither Pramanik et al. or Blattner et al. teach or suggest determining open reading frames of genes having an unknown function and assigning a function to their encoded products based on homology to proteins in a different organism. The combination of Pramanik et al. and Blattner et al. also fails to provide the requisite motivation to arrive at Applicant's claimed invention.

Pramanik et al. describe construction of a metabolic model using only biochemical data. While Pramanik et al. list some genes, the list is incomplete compared to the model and consists only of known genes encoding proteins with a known biochemical activity. There is no teaching, suggestion or motivation to create a model using open reading frames of genes of unknown function. Blattner et al. merely report on the *E. coli* genome sequencing and also fail to provide any teaching, suggestion or motivation to combine genome sequence information with the biochemically-based model of Pramanik et al. Blattner et al. teach that 38% of the protein-coding genes have no attributable function (abstract, lines 1-2; page 1458, col. 3, para. 1, lines 1-9, and Table 4) and that nearly 60% of *E. coli* proteins have no match in any other complete genome that was considered (page 1459, col. 2, para. 2, lines 1-3). Because Pramanik et al. teach the construction of models from biochemical information and Blattner et al. describe that more than one third of the *E. coli* genome could not be attributed a function and that close to two thirds have no match in another organism, the combination of Pramanik et al. and Blattner et al. would not lead one skilled in the art to construct an *in silico* strain by determining open reading frames of unknown function and assign a function to the encoded protein by homology to a gene in a different organism as claimed. Accordingly, the cited combination cannot render the invention obvious as claimed and withdrawal of this ground of rejection is respectfully requested.

Claim 64 stands rejected under 35 U.S.C. § 103(a) as allegedly obvious over Pramanik et al., *supra*, in view of Blattner et al., *supra*, and further in view of Xie et al., TIBTECH 15:109-

113 (1997). As discussed above, neither of Pramanik et al., alone or in combination with Blattner et al., teaches or suggest Applicant's claimed methods. Moreover, Xie et al. fails to cure the deficiencies of these references. At best, Xie et al. describes the design of media and feeding strategies for fed-batch cultures of animal cells. However, Xie et al. provides no teaching or suggestion, alone or when combined with Pramanik et al. and/or Blattner et al., of the claimed methods of determining opening reading frames of genes of unknown function and assigning function to them based on homology to genes in a different organism. Accordingly, Applicant submits that the invention as claimed is unobvious over the cited art. Therefore, withdrawal of this ground of rejection is respectfully requested.

CONCLUSION

In light of the amendments and remarks herein, Applicant submits that the claims are now in condition for allowance and respectfully requests a notice to this effect. The Examiner is invited to call the undersigned if there are any questions.

To the extent necessary, a petition for an extension of time under 37 C.F.R. 1.136 is hereby made. Please charge any shortage in fees due in connection with the filing of this paper, including extension of time fees, to Deposit Account 502624 and please credit any excess fees to such deposit account.

Respectfully submitted,

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